BLAST ® » blastn suite » results for RID-S4KAVS04015

Job Title	Nucleotide Sequence ...
RID	S4KAVS04015 Search expires on 09-19 23:29 pm
Program	BLASTN
Database	nr
Query ID	lcl|Query_221305
Description	None ...
Molecule type	dna
Query Length	1121

Descriptions

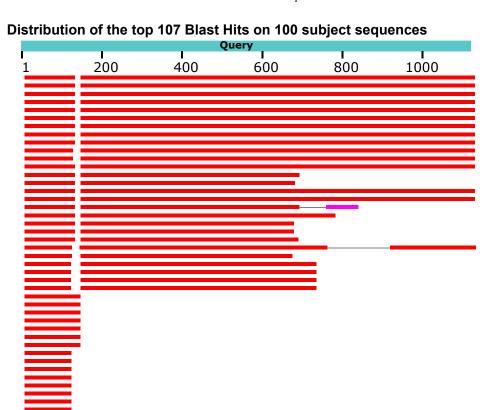| Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630017O09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1748	1748	87%	0.0	98.78%	AK154309.1
PREDICTED: Mus musculus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1629	1629	87%	0.0	96.85%	XM_006510253.2
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Sc5d:tm1a(EUCOMM)Hmgu; transgenic	1629	1765	87%	0.0	96.85%	JN961338.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Sc5d:tm1e(EUCOMM)Hmgu; transgenic	1629	1765	87%	0.0	96.85%	JN951773.1
Mus musculus sterol-C5-desaturase (Sc5d), mRNA	1629	1629	87%	0.0	96.85%	NM_172769.2
Mus musculus BAC clone RP24-395P13 from chromosome 9, complete sequence	1629	1875	87%	0.0	96.85%	AC160051.2
Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730515E09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1629	1629	87%	0.0	96.85%	AK077670.1
Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830037K02 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1629	1629	87%	0.0	96.85%	AK043825.1
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X3, mRNA	1474	1474	87%	0.0	94.00%	XM_029481771.1
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	1474	1474	87%	0.0	94.00%	XM_021172472.2
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1474	1474	87%	0.0	94.00%	XM_021172471.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1046	1046	87%	0.0	87.00%	XM_021207205.2
Mus musculus C5D mRNA for sterol-C5-desaturase, complete cds	979	979	48%	0.0	99.44%	AB016248.1
Mus musculus sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), mRNA (cDNA clone MGC:37898 IMAGE:5101986), complete cds	977	977	47%	0.0	100.00%	BC024132.1
PREDICTED: Rattus norvegicus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	723	723	87%	0.0	81.10%	XM_017595406.1
Rattus norvegicus sterol-C5-desaturase (Sc5d), mRNA	723	723	87%	0.0	81.10%	NM_053642.2
Mus musculus BAC clone RP23-346J12 from chromosome 6, complete sequence	702	787	55%	0.0	90.04%	AC122333.2
PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	699	699	56%	0.0	87.84%	XM_021207206.2
Mus musculus predicted gene, 31520 (Gm31520), non-coding RNA	678	678	47%	0.0	89.80%	NR_136927.1
Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830041I17 product:weakly similar to STEROL C5-DESATURASE [Rattus norvegicus], full insert sequence	678	678	47%	0.0	89.80%	AK052921.1
PREDICTED: Mus pahari lathosterol oxidase-like (LOC110334695), mRNA	579	579	47%	1e-160	87.25%	XM_029547953.1
PREDICTED: Mesocricetus auratus sterol-C5-desaturase (Sc5d), mRNA	424	635	73%	6e-114	79.62%	XM_005069403.3
Rattus norvegicus C5D mRNA for sterol C5-desaturase, complete cds	407	407	46%	6e-109	81.46%	AB052846.1
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	396	396	52%	1e-105	79.44%	XM_007651891.3
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	396	396	52%	1e-105	79.44%	XM_003511371.4
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	392	392	52%	2e-104	79.30%	XM_027411877.1
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	392	392	52%	2e-104	79.30%	XM_027411876.1
RNA interference vector psiCHECK(TM)-2, complete sequence	252	252	12%	3e-62	100.00%	AY535007.1
RNA interference vector psiCHECK(TM)-1, complete sequence	252	252	12%	3e-62	100.00%	AY535006.1
Co-reporter vector phRL-CMV, complete sequence	231	231	12%	4e-56	97.10%	AF362549.1
Co-reporter vector phRL-SV40, complete sequence	231	231	12%	4e-56	97.10%	AF362548.1
Co-reporter vector phRL-TK(Int-), complete sequence	231	231	12%	4e-56	97.10%	AF362547.1
Co-reporter vector phRL-null, complete sequence	231	231	12%	4e-56	97.10%	AF362546.1
Co-reporter vector pHRL-TK, complete sequence	231	231	12%	4e-56	97.10%	AF362545.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Renilla luciferase reporter vector pGL4.75[hRluc/CMV], complete sequence	228	228	10%	5e-55	100.00%	AY738231.1
Renilla luciferase reporter vector pGL4.74[hRluc/TK], complete sequence	228	228	10%	5e-55	100.00%	AY738230.1
Renilla luciferase reporter vector pGL4.73[hRluc/SV40], complete sequence	228	228	10%	5e-55	100.00%	AY738229.1
Renilla luciferase reporter vector pGL4.70[hRluc], complete sequence	228	228	10%	5e-55	100.00%	AY738226.1
Co-reporter vector phRG-TK, complete sequence	228	228	10%	5e-55	100.00%	AF362551.1
Co-reporter vector phRG-B, complete sequence	228	228	10%	5e-55	100.00%	AF362550.1
Synthetic Renilla luciferase reporter vector pGL4.82[hRluc/Puro], complete sequence	228	228	10%	5e-55	100.00%	DQ188846.1
Renilla luciferase reporter vector pGL4.79[hRluc/Neo], complete sequence	228	228	10%	5e-55	100.00%	DQ188843.1
Luciferase reporter vector pGL4.76[hRluc/Hygro], complete sequence	228	228	10%	5e-55	100.00%	AY864931.1
Cloning vector pT7 RL2, complete sequence	217	217	10%	1e-51	100.00%	KM099240.1
Cloning vector pT7_RL1, complete sequence	217	217	10%	1e-51	100.00%	KM099239.1
Renilla luciferase reporter vector pGL4.72[hRlucCP], complete sequence	217	217	10%	1e-51	99.17%	AY738228.1
Renilla luciferase reporter vector pGL4.71[hRlucP], complete sequence	217	217	10%	1e-51	99.17%	AY738227.1
Reporter vector phRG(R2.2), complete sequence	217	217	10%	1e-51	99.17%	AY487824.1
Reporter vector phRG(R2.1), complete sequence	217	217	10%	1e-51	99.17%	AY487823.1
Synthetic Renilla luciferase reporter vector pGL4.84[hRlucCP/Puro], complete sequence	217	217	10%	1e-51	99.17%	DQ188848.1
Synthetic Renilla luciferase reporter vector pGL4.83[hRlucP/Puro], complete sequence	217	217	10%	1e-51	99.17%	DQ188847.1
Synthetic Renilla luciferase reporter vector pGL4.81[hRlucCP/Neo], complete sequence	217	217	10%	1e-51	99.17%	DQ188845.1
Synthetic Renilla luciferase reporter vector pGL4.80[hRlucP/Neo], complete sequence	217	217	10%	1e-51	99.17%	DQ188844.1
Luciferase reporter vector pGL4.78[hRlucCP/Hygro], complete sequence	217	217	10%	1e-51	99.17%	AY864933.1
Luciferase reporter vector pGL4.77[hRlucP/Hygro], complete sequence	217	217	10%	1e-51	99.17%	AY864932.1
Plant expression vector pDuExB2 (pDuExD7), complete sequence	213	425	10%	1e-50	100.00%	EF565885.1
Plant expression vector pDuExB (pDuExDc6), complete sequence	213	213	10%	1e-50	100.00%	EF565884.1
Synthetic construct clone Den3-E24 Rluc-ubiquitin-neo fusion protein and polyprotein genes, complete cds	211	211	10%	5e-50	100.00%	KM222446.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Synthetic construct clone Den3-E21 Rluc-ubiquitin-neo fusion protein and polyprotein genes, complete cds	211	211	10%	5e-50	100.00%	KM222445.1
Cloning vector pCRm-Rluc-PHLEO, complete sequence	211	211	10%	5e-50	100.00%	KF035117.1
Cloning vector pCRm-Rluc-PAC, complete sequence	211	211	10%	5e-50	100.00%	KF035116.1
Cloning vector pCRm-Rluc-NEO, complete sequence	211	211	10%	5e-50	100.00%	KF035115.1
Cloning vector pCRm-Rluc-HYG, complete sequence	211	211	10%	5e-50	100.00%	KF035114.1
Cloning vector pCRm-Rluc-BSD, complete sequence	211	211	10%	5e-50	100.00%	KF035113.1
Hepatitis C virus replicon 4a ED43-RlucNeo (R+I), complete sequence	211	211	10%	5e-50	100.00%	JX885981.1
Biobrick cloning vector BBa_J96034, complete sequence	211	211	10%	5e-50	100.00%	JN204887.1
Cloning vector pDuExDn6, complete sequence	211	211	10%	5e-50	100.00%	GU370779.1
Cloning vector pBIND-GR, complete sequence	211	211	10%	5e-50	100.00%	GQ229580.1
Cloning vector pBIND-ER (alpha), complete sequence	211	211	10%	5e-50	100.00%	GQ229579.1
Cloning vector pFN26A (BIND) hRluc-neo, complete sequence	211	211	10%	5e-50	100.00%	GQ229578.1
Cloning vector pmirGLO, complete sequence	211	211	10%	5e-50	100.00%	FJ376737.1
CMV hRluc-neo Flexi Vector pF9A, complete sequence	211	211	10%	5e-50	100.00%	DQ871024.1
Synthetic construct gene for mKusabiraOrangeKappa-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	LC033422.1
Synthetic construct gene for mKusabiraOrange1-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	LC033416.1
Synthetic construct gene for mCherry(delC13)-RLuc8.6(delN6), complete cds	206	206	10%	2e-48	98.29%	LC033414.1
Synthetic construct gene for mCherry(delC13)-RLuc8.6(delN5), complete cds	206	206	10%	2e-48	98.29%	LC033413.1
Synthetic construct gene for mCherry(delC13)-RLuc8.6(delN4), complete cds	206	206	10%	2e-48	98.29%	LC033412.1
Synthetic construct gene for mCherry(delC12)-RLuc8.6(delN6), complete cds	206	206	10%	2e-48	98.29%	LC033411.1
Synthetic construct gene for mCherry(delC12)-RLuc8.6(delN5), complete cds	206	206	10%	2e-48	98.29%	LC033410.1
Synthetic construct gene for mCherry(delC12)-RLuc8.6(delN4), complete cds	206	206	10%	2e-48	98.29%	LC033409.1
Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6(delN6), complete cds	206	206	10%	2e-48	98.29%	LC033408.1
Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6(delN5), complete cds	206	206	10%	2e-48	98.29%	LC033407.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6(delN4), complete cds	206	206	10%	2e-48	98.29%	LC033406.1
Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	LC033405.1
Synthetic construct gene for mCherry(delC10)-Orange-Nano-lantern, complete cds	206	206	10%	2e-48	98.29%	LC033404.1
Synthetic construct gene for Che(dC10-sC2)-RL8m1, complete cds	206	206	10%	2e-48	98.29%	LC033401.1
Synthetic construct gene for Che(dC10-sC1)-RL8m1, complete cds	206	206	10%	2e-48	98.29%	LC033400.1
Synthetic construct gene for Orange-Nano-lantern(Ca2+)-H2B, complete cds	206	206	10%	2e-48	97.50%	AB983217.1
Synthetic construct gene for Orange-Nano-lantern(Ca2+), complete cds	206	206	10%	2e-48	98.29%	AB983216.1
Synthetic construct gene for TurboFP650-RLuc8.6-545, complete cds	206	206	10%	2e-48	98.29%	AB982104.1
Synthetic construct gene for TurboFP635-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	AB982103.1
Synthetic construct gene for TurboFP635-RLuc8.6-545, complete cds	206	206	10%	2e-48	98.29%	AB982102.1
Synthetic construct gene for tdTomato-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	AB982100.1
Synthetic construct gene for TagRFP-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	AB982098.1
Synthetic construct gene for mRuby2-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	AB982096.1
Synthetic construct gene for mOrange2-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	AB982095.1
Synthetic construct gene for mKusabiraOrange2(delC5)-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	AB982094.1
Synthetic construct gene for mKusabiraOrange2(delC4)-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	AB982093.1
Synthetic construct gene for mKusabiraOrange2(delC3)-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	AB982092.1
Synthetic construct gene for mKusabiraOrange2(delC2)-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	AB982091.1

Graphic Summary

Distribution of the top 107 Blast Hits on 100 subject sequences

Alignments

Alignment view [Pairwise ▲▼]   ☐ CDS feature

Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630017O09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence
Sequence ID: **AK154309.1** Length: 2251 Number of Matches: 1
Range 1: 1101 to 2087

Score	Expect	Identities	Gaps	Strand	Frame
1748 bits(946)	0.0()	975/987(99%)	10/987(1%)	Plus/Plus	

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Query  145   GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT  204
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Sbjct  1101  GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT  1160

Query  205   AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC  264
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Sbjct  1161  AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC  1220

Query  265   AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT  324
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Sbjct   1221   AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT   1280

Query    325   AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT    384
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Sbjct   1281   AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT   1340

Query    385   GCATACTCATTAAGGaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA    444
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Sbjct   1341   GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA   1400

Query    445   ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA    504
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Sbjct   1401   ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA   1460

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Sbjct   1461   GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG   1520

Query    565   TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT    624
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Sbjct   1521   TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT   1580

Query    625   TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTAttttttttAAA    684
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Sbjct   1581   TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTATTTTTTTTTAAA   1640

Query    685   TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG    744
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1641   TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG   1700

Query    745   AGTGTCAttttttttttctttctttttttttttttttttttttttG----GG-TTTTTAAGACAG    799
               ||||||| |||||| |||| ||||||||||||||||||||||||  ||  || ||||||||||||
Sbjct   1701   AGTGTCATTTTTTTTTTCTTTCTTTTTTTTTTTTTTTTTTTTTTTTGGTTTTTTAAGACAG   1760

Query    800   GGTTTCTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTC    859
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1761   GGTTTCTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTC   1820

Query    860   AGAGATCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGATGT    919
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1821   AGAGATCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGATGT   1880

Query    920   GTGTCATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTA    979
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Sbjct   1881   GTGTCATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTA   1940

Query    980   TAAACTTGTGGCACCCAGTGACATCttttttttAATCAAGTGGACACACTTTTGATGTATT   1039
               |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct   1941   TAAACTTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTGATGTATT   2000

Query   1040   TCTCAGTTACAAAGCTGACTTTTTT-AATGAAGGGAA-AATTGCCA-GTACTT-AATCTA   1095
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Sbjct   2001   TCTCAGTTACAAAGCTGACTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTA   2060

Query   1096   CCTAAGGTACACTTTAGACC-CATCTT   1121
               |||||||||||||||||||| ||||||
Sbjct   2061   CCTAAGGTACACTTTAGACCTCATCTT   2087
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PREDICTED: Mus musculus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA
Sequence ID: **XM_006510253.2** Length: 4826 Number of Matches: 1
Range 1: 1146 to 2118

Score	Expect	Identities	Gaps	Strand	Frame
1629 bits(882)	0.0()	953/984(97%)	18/984(1%)	Plus/Plus	

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Query    145   GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT    204
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Sbjct   1146   GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT   1205

Query    205   AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC    264
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1206   AAACAGCGGGAAGACACCGGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC   1265

Query    265   AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT    324
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1266   AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT   1325

Query    325   AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT    384
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Sbjct   1326   AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT   1385

Query    385   GCATACTCATTAAGGaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA    444
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1386   GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA   1445
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Query  445   ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA   504
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Sbjct  1446  ACCCTAACGATGAAGATGGTCCTGTCCCGGGAGCGGCTGGCTCCACCGAAGTGCTGGGGA   1505

Query  505   GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG   564
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  1506  GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAGCTGATACGTGAGTGGCAG   1565

Query  565   TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT   624
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1566  TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT   1625

Query  625   TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTAtttttttttAAA   684
             |||||||||||||||||||||||||||||||||||||||||||||||||        |||
Sbjct  1626  TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTATTTTTTTTTAAA   1685

Query  685   TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG   744
             |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Sbjct  1686  TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG   1743

Query  745   AGTGTCAtttttttttctttcttttttttttttttttttttGGGTTTTTAAGACAGGGTTT   804
             ||||||| ||||||||| ||| |||||||||        |||||||| ||||||||||||
Sbjct  1744  AGTGTCATTTTTTTTTTCTTT-TTTCTTTTTTTT--------GGTTTTTCAAGACAGGGTTT   1794

Query  805   CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA   864
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1795  CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA   1854

Query  865   TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGATGTGTGTC   924
             ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  1855  TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGAAGTGTGTC   1914

Query  925   ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC   984
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1915  ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC   1974

Query  985   TTGTGGCACCCAGTGACATCtttttttAATCAAGTGGACACACTTTTGATGTATTTCTCA   1044
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  1975  TTGTGGCACCCAGTGACATCTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA   2034

Query  1045  GTTACAAAGCTGACTTTTTT--AATGAAGGGAA-AATTGCCA-GTACTT-AATCTACCTA   1099
             ||||||||||||||||||||  |||| |||||| |||||||| ||||||  |||||||||
Sbjct  2035  GTTACAAAGCTGACTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG   2094

Query  1100  AGGTACACTTT-AGACC-CATCTT   1121
             |||||||||||  ||||  ||||||
Sbjct  2095  AGGTACACTTTTAAACCTCATCTT   2118
```

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Sc5d:tm1a(EUCOMM)Hmgu; transgenic
Sequence ID: **JN961338.1** Length: 38137 Number of Matches: 2
Range 1: 26029 to 27001

Score	Expect	Identities	Gaps	Strand	Frame
1629 bits(882)	0.0()	953/984(97%)	18/984(1%)	Plus/Plus	

```
Query  145    GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT   204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26029  GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT   26088

Query  205    AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC   264
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  26089  AAACAGCGGGAAGACACCGGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC   26148

Query  265    AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT   324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26149  AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT   26208

Query  325    AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT   384
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  26209  AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT   26268

Query  385    GCATACTCATTAAGGaaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA   444
              |||||||||||||||        ||||||||||||||||||||||||||||||||||||||
Sbjct  26269  GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA   26328

Query  445    ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA   504
              |||||||  |||||||||| |||||||||  |||||| ||||||||||||| |||||||||
Sbjct  26329  ACCCTAACGATGAAGATGGTCCTGTCCCGGGAGCGGCTGGCTCCACCGAAGTGCTGGGGA   26388

Query  505    GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG   564
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  26389  GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAGCTGATACGTGAGTGGCAG   26448
```

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Query   565    TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT   624
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   26449  TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT   26508

Query   625    TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTAtttttttttAAA   684
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   26509  TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTATTTTTTTTTAAA   26568

Query   685    TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG   744
               ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Sbjct   26569  TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG   26626

Query   745    AGTGTCAtttttttttctttctttttttttttttttttttttGGGTTTTTAAGACAGGGTTT   804
               ||||||| ||||||||| |||| ||||||||||        ||||||| ||||||||||||
Sbjct   26627  AGTGTCATTTTTTTTTTCTTT-TTTCTTTTTTT--------GGTTTTTCAAGACAGGGTTT   26677

Query   805    CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA   864
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   26678  CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA   26737

Query   865    TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGATGTGTGTC   924
               |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct   26738  TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGAAGTGTGTC   26797

Query   925    ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC   984
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   26798  ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC   26857

Query   985    TTGTGGCACCCAGTGACATCtttttttAATCAAGTGGACACACTTTTGATGTATTTCTCA   1044
               ||||||||||||||||||||       |||||||||||||||||||||||||||||||||
Sbjct   26858  TTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA   26917

Query   1045   GTTACAAAGCTGACTTTTTT--AATGAAGGGAA-AATTGCCA-GTACTT-AATCTACCTA   1099
               |||||||||||||||||||   |||||||||| |||||||| ||||||  ||||||||||
Sbjct   26918  GTTACAAAGCTGACTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG   26977

Query   1100   AGGTACACTTT-AGACC-CATCTT   1121
               |||||||||||  |||| ||||||
Sbjct   26978  AGGTACACTTTTAAACCTCATCTT   27001
```

Range 2: 37078 to 37200

Score	Expect	Identities	Gaps	Strand	Frame
135 bits(73)	3e-27()	107/123(87%)	4/123(3%)	Plus/Plus	

```
Query   756    tttttctttctttttttttttttttttttttttGGGTTTTTAAGACAGGGTTTCTCTGTGTAGC   815
               ||||| ||| ||| ||| |||||| ||| ||||| | ||||||||||||||||||||||||||
Sbjct   37078  TTTTTGTTTTTTGTTTTTTTGTTTTGTTTTGTTTTTTAAGACAGGGTTTCTCTGTGTAGC   37137

Query   816    CCTGGCTGTCCTGGAACTC--T--GTAGACTGGGCTGGCCTCGAACTCAGAGATCTGCCT   871
               |||||||||||||||||||  |  ||||||||||||||||||||||||||||| ||||||
Sbjct   37138  CCTGGCTGTCCTGGAGCTCACTTTGTAGATCAGGCTGGCCTCGAACTCAGAAATCTGCCT   37197

Query   872    GCC   874
               |||
Sbjct   37198  GCC   37200
```

Mus musculus targeted non-conditional, lacZ-tagged mutant allele Sc5d:tm1e(EUCOMM)Hmgu; transgenic
Sequence ID: **JN951773.1** Length: 38097 Number of Matches: 2
Range 1: 25989 to 26961

Score	Expect	Identities	Gaps	Strand	Frame
1629 bits(882)	0.0()	953/984(97%)	18/984(1%)	Plus/Plus	

```
Query   145    GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT   204
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   25989  GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT   26048

Query   205    AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC   264
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   26049  AAACAGCGGGAAGACACCGGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC   26108

Query   265    AGGAACAACTTGTCTTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT   324
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   26109  AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT   26168

Query   325    AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT   384
               |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct   26169  AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT   26228
```

```
Query  385    GCATACTCATTAAGGaaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA  444
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26229  GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA   26288

Query  445    ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA  504
              ||||||| |||||||||||| ||||||||| |||||||||||||||||||| ||||||||
Sbjct  26289  ACCCTAACGATGAAGATGGTCCTGTCCCCGGGAGCGGCTGGCTCCACCGAAGTGCTGGGGA  26348

Query  505    GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG  564
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  26349  GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAGCTGATACGTGAGTGGCAG   26408

Query  565    TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT  624
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26409  TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT   26468

Query  625    TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTAttttttttAAA  684
              |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26469  TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTATTTTTTTTTAAA  26528

Query  685    TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG  744
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Sbjct  26529  TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG   26586

Query  745    AGTGTCAtttttttttctttctttttttttttttttttttttGGGTTTTTAAGACAGGGTTT  804
              |||||||                                    |||||| ||||||||||||
Sbjct  26587  AGTGTCATTTTTTTTTTCTTT-TTTCTTTTTTT--------GGTTTTTCAAGACAGGGTTT   26637

Query  805    CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA  864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26638  CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA   26697

Query  865    TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGATGTGTGTC  924
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  26698  TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGAAGTGTGTC   26757

Query  925    ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC  984
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26758  ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC   26817

Query  985    TTGTGGCACCCAGTGACATCtttttttAATCAAGTGGACACACTTTTGATGTATTTCTCA  1044
              ||||||||||||||||||||       |||||||||||||||||||||||||||||||||
Sbjct  26818  TTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA  26877

Query  1045   GTTACAAAGCTGACTTTTTT--AATGAAGGGAA-AATTGCCA-GTACTT-AATCTACCTA  1099
              ||||||||||||||||||||  ||||||||||| ||||||||  |||||  |||||||||
Sbjct  26878  GTTACAAAGCTGACTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG   26937

Query  1100   AGGTACACTTT-AGACC-CATCTT  1121
              |||||||||||  |||  ||||||
Sbjct  26938  AGGTACACTTTTAAACCTCATCTT   26961
```

Range 2: 37038 to 37160

Score	Expect	Identities	Gaps	Strand	Frame
135 bits(73)	3e-27()	107/123(87%)	4/123(3%)	Plus/Plus	

```
Query  756    tttttctttctttttttttttttttttttttGGGTTTTTAAGACAGGGTTTCTCTGTGTAGC  815
              ||||| |||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  37038  TTTTTGTTTTTTGTTTTTTTTGTTTTGTTTTGTTTTTTAAGACAGGGTTTCTCTGTGTAGC  37097

Query  816    CCTGGCTGTCCTGGAACTC--T--GTAGACTGGGCTGGCCTCGAACTCAGAGATCTGCCT  871
              |||||||||||||||| |||      |||||||||||||||||||||||||||| ||||||
Sbjct  37098  CCTGGCTGTCCTGGAGCTCACTTTGTAGATCAGGCTGGCCTCGAACTCAGAAATCTGCCT   37157

Query  872    GCC  874
              |||
Sbjct  37158  GCC  37160
```

Mus musculus sterol-C5-desaturase (Sc5d), mRNA
Sequence ID: **NM_172769.2** Length: 2249 Number of Matches: 1
Range 1: 1154 to 2126

Score	Expect	Identities	Gaps	Strand	Frame
1629 bits(882)	0.0()	953/984(97%)	18/984(1%)	Plus/Plus	

```
Query  145    GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT  204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1154   GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTCATGCTGAGGGATGGTCCTGACAGT  1213
```

```
Query   205   AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC   264
              ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct   1214  AAACAGCGGGAAGACACCGGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC   1273

Query   265   AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT   324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1274  AGGAACAACTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT   1333

Query   325   AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT   384
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct   1334  AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT   1393

Query   385   GCATACTCATTAAGGaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA   444
              |||||||||||||||       |||||||||||||||||||||||||||||||||||||
Sbjct   1394  GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA   1453

Query   445   ACCCTAAAGATGAAGATGTTCCTGTCCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA   504
              ||||||| ||||||||||| |||||||| |||||||||||||||||||| ||||||||||
Sbjct   1454  ACCCTAACGATGAAGATGGTCCTGTCCCGGGAGCGGCTGGCTCCACCGAAGTGCTGGGGA   1513

Query   505   GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG   564
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct   1514  GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAGCTGATACGTGAGTGGCAG   1573

Query   565   TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT   624
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1574  TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT   1633

Query   625   TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTAttttttttAAA   684
              |||||||||||||||||||||||||||||||||||||||||||||||||        |||
Sbjct   1634  TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTATTTTTTTTAAA   1693

Query   685   TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG   744
              |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Sbjct   1694  TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG   1751

Query   745   AGTGTCAttttttttttctttcttttttttttttttttttttGGGTTTTTAAGACAGGGTTT   804
              ||||||| |||||||| |||| |||||||||         |||||||| |||||||||||
Sbjct   1752  AGTGTCATTTTTTTTTCTTT-TTTCTTTTTTTT--------GGTTTTTCAAGACAGGGTTT   1802

Query   805   CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA   864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1803  CTCTGTGTAGCCCTGGCTGTCCTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAGAGA   1862

Query   865   TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGATGTGTGTC   924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct   1863  TCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACTGCCCAGCTTGAAGTGTGTC   1922

Query   925   ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC   984
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1923  ATTTAAAACCACTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATAAAC   1982

Query   985   TTGTGGCACCCAGTGACATCtttttttAATCAAGTGGACACACTTTTGATGTATTTCTCA   1044
              ||||||||||||||||||||       |||||||||||||||||||||||||||||||||
Sbjct   1983  TTGTGGCACCCAGTGACATCTTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTCTCA   2042

Query   1045  GTTACAAAGCTGACTTTTTT--AATGAAGGGAA-AATTGCCA-GTACTT-AATCTACCTA   1099
              |||||||||||||||||||   |||||||||| ||||||||  |||||  ||||||||
Sbjct   2043  GTTACAAAGCTGACTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTACCTG   2102

Query   1100  AGGTACACTTT-AGACC-CATCTT     1121
              ||||||||||| ||||| ||||||
Sbjct   2103  AGGTACACTTTTAAACCTCATCTT     2126
```

Taxonomy

Reports

- ### Lineage

Organism	Blast Name	Score	Number of Hits	Description
root			101	
.Muroidea	rodents		28	
..Murinae	rodents		23	
...Mus	rodents		19	
....Mus	rodents		16	

.....Mus musculus	rodents	1748	13	**Mus musculus hits**
.....Mus caroli	rodents	1474	3	**Mus caroli hits**
....Mus pahari	rodents	1046	3	**Mus pahari hits**
...Rattus norvegicus	rodents	723	4	**Rattus norvegicus hits**
..Mesocricetus auratus	rodents	424	1	**Mesocricetus auratus hits**
..Cricetulus griseus	rodents	396	4	**Cricetulus griseus hits**
.RNA interference vector psiCHECK(TM)-2	other sequences	252	1	**RNA interference vector psiCHECK(TM)-2 hits**
.RNA interference vector psiCHECK(TM)-1	other sequences	252	1	**RNA interference vector psiCHECK(TM)-1 hits**
.Co-reporter vector phRL-CMV	other sequences	231	1	**Co-reporter vector phRL-CMV hits**
.Co-reporter vector phRL-SV40	other sequences	231	1	**Co-reporter vector phRL-SV40 hits**
.Co-reporter vector phRL-TK(Int-)	other sequences	231	1	**Co-reporter vector phRL-TK(Int-) hits**
.Co-reporter vector phRL-null	other sequences	231	1	**Co-reporter vector phRL-null hits**
.Co-reporter vector pHRL-TK	other sequences	231	1	**Co-reporter vector pHRL-TK hits**
.Renilla luciferase reporter vector pGL4.75[hRluc/CMV]	other sequences	228	1	**Renilla luciferase reporter vector pGL4.75[hRluc/CMV] hits**
.Renilla luciferase reporter vector pGL4.74[hRluc/TK]	other sequences	228	1	**Renilla luciferase reporter vector pGL4.74[hRluc/TK] hits**
.Renilla luciferase reporter vector pGL4.73[hRluc/SV40]	other sequences	228	1	**Renilla luciferase reporter vector pGL4.73[hRluc/SV40] hits**
.Renilla luciferase reporter vector pGL4.70[hRluc]	other sequences	228	1	**Renilla luciferase reporter vector pGL4.70[hRluc] hits**
.Co-reporter vector phRG-TK	other sequences	228	1	**Co-reporter vector phRG-TK hits**
.Co-reporter vector phRG-B	other sequences	228	1	**Co-reporter vector phRG-B hits**
.Renilla luciferase reporter vector pGL4.82[hRluc/Puro]	other sequences	228	1	**Renilla luciferase reporter vector pGL4.82[hRluc/Puro] hits**
.Renilla luciferase reporter vector pGL4.79[hRluc/Neo]	other sequences	228	1	**Renilla luciferase reporter vector pGL4.79[hRluc/Neo] hits**
.Luciferase reporter vector pGL4.76[hRluc/Hygro]	other sequences	228	1	**Luciferase reporter vector pGL4.76[hRluc/Hygro] hits**
.Cloning vector pT7 RL2	other sequences	217	1	**Cloning vector pT7 RL2 hits**
.Cloning vector pT7_RL1	other sequences	217	1	**Cloning vector pT7_RL1 hits**
.Renilla luciferase reporter vector pGL4.72[hRlucCP]	other sequences	217	1	**Renilla luciferase reporter vector pGL4.72[hRlucCP] hits**
.Renilla luciferase reporter vector pGL4.71[hRlucP]	other sequences	217	1	**Renilla luciferase reporter vector pGL4.71[hRlucP] hits**
.Reporter vector phRG(R2.2)	other sequences	217	1	**Reporter vector phRG(R2.2) hits**
.Reporter vector phRG(R2.1)	other sequences	217	1	**Reporter vector phRG(R2.1) hits**
.Renilla luciferase reporter vector pGL4.84[hRlucCP/Puro]	other sequences	217	1	**Renilla luciferase reporter vector pGL4.84[hRlucCP/Puro] hits**
.Renilla luciferase reporter vector pGL4.83[hRlucP/Puro]	other sequences	217	1	**Renilla luciferase reporter vector pGL4.83[hRlucP/Puro] hits**
.Renilla luciferase reporter vector pGL4.81[hRlucCP/Neo]	other sequences	217	1	**Renilla luciferase reporter vector pGL4.81[hRlucCP/Neo] hits**

.Renilla luciferase reporter vector pGL4.80[hRlucP/Neo]	other sequences	217	1	**Renilla luciferase reporter vector pGL4.80[hRlucP/Neo] hits**
.Luciferase reporter vector pGL4.78[hRlucCP/Hygro]	other sequences	217	1	**Luciferase reporter vector pGL4.78[hRlucCP/Hygro] hits**
.Luciferase reporter vector pGL4.77[hRlucP/Hygro]	other sequences	217	1	**Luciferase reporter vector pGL4.77[hRlucP/Hygro] hits**
.Plant expression vector pDuExB2 (pDuExD7)	other sequences	213	1	**Plant expression vector pDuExB2 (pDuExD7) hits**
.Plant expression vector pDuExB (pDuExDc6)	other sequences	213	1	**Plant expression vector pDuExB (pDuExDc6) hits**
.synthetic construct	other sequences	211	30	**synthetic construct hits**
.Cloning vector pCRm-Rluc-PHLEO	other sequences	211	1	**Cloning vector pCRm-Rluc-PHLEO hits**
.Cloning vector pCRm-Rluc-PAC	other sequences	211	1	**Cloning vector pCRm-Rluc-PAC hits**
.Cloning vector pCRm-Rluc-NEO	other sequences	211	1	**Cloning vector pCRm-Rluc-NEO hits**
.Cloning vector pCRm-Rluc-HYG	other sequences	211	1	**Cloning vector pCRm-Rluc-HYG hits**
.Cloning vector pCRm-Rluc-BSD	other sequences	211	1	**Cloning vector pCRm-Rluc-BSD hits**
.Hepatitis C virus replicon 4a ED43-RlucNeo (R+I)	other sequences	211	1	**Hepatitis C virus replicon 4a ED43-RlucNeo (R+I) hits**
.Biobrick cloning vector BBa_J96034	other sequences	211	1	**Biobrick cloning vector BBa_J96034 hits**
.Cloning vector pDuExDn6	other sequences	211	1	**Cloning vector pDuExDn6 hits**
.Cloning vector pBIND-GR	other sequences	211	1	**Cloning vector pBIND-GR hits**
.Cloning vector pBIND-ER (alpha)	other sequences	211	1	**Cloning vector pBIND-ER (alpha) hits**
.Cloning vector pFN26A (BIND) hRluc-neo	other sequences	211	1	**Cloning vector pFN26A (BIND) hRluc-neo hits**
.Cloning vector pmirGLO	other sequences	211	1	**Cloning vector pmirGLO hits**
.CMV hRluc-neo Flexi Vector pF9A	other sequences	211	1	**CMV hRluc-neo Flexi Vector pF9A hits**

○ **Organism**

Description	Score	E value	Accession
Mus musculus (house mouse) [rodents]			
Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630017O09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1748	0.0	AK154309
PREDICTED: Mus musculus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1629	0.0	XM_006510253
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Sc5d:tm1a(EUCOMM)Hmgu; transgenic	1629	0.0	JN961338
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Sc5d:tm1e(EUCOMM)Hmgu; transgenic	1629	0.0	JN951773
Mus musculus sterol-C5-desaturase (Sc5d), mRNA	1629	0.0	NM_172769
Mus musculus BAC clone RP24-395P13 from chromosome 9, complete sequence	1629	0.0	AC160051

Description	Score	E value	Accession
Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730515E09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1629	0.0	AK077670
Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830037K02 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence	1629	0.0	AK043825
Mus musculus C5D mRNA for sterol-C5-desaturase, complete cds	979	0.0	AB016248
Mus musculus sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), mRNA (cDNA clone MGC:37898 IMAGE:5101986), complete cds	977	0.0	BC024132
Mus musculus BAC clone RP23-346J12 from chromosome 6, complete sequence	702	0.0	AC122333
Mus musculus predicted gene, 31520 (Gm31520), non-coding RNA	678	0.0	NR_136927
Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830041I17 product:weakly similar to STEROL C5-DESATURASE [Rattus norvegicus], full insert sequence	678	0.0	AK052921
Mus caroli (Ryukyu mouse) [rodents]			
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X3, mRNA	1474	0.0	XM_029481771
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	1474	0.0	XM_021172472
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1474	0.0	XM_021172471
Mus pahari (shrew mouse) [rodents]			
PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1046	0.0	XM_021207205
PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	699	0.0	XM_021207206
PREDICTED: Mus pahari lathosterol oxidase-like (LOC110334695), mRNA	579	1e-160	XM_029547953
Rattus norvegicus (Norway rat) [rodents]			
PREDICTED: Rattus norvegicus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	723	0.0	XM_017595406
Rattus norvegicus sterol-C5-desaturase (Sc5d), mRNA	723	0.0	NM_053642
Rattus norvegicus sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like, mRNA (cDNA clone MGC:93101 IMAGE:7131154), complete cds	723	0.0	BC081704
Rattus norvegicus C5D mRNA for sterol C5-desaturase, complete cds	407	6e-109	AB052846
Mesocricetus auratus (golden hamster) [rodents]			
PREDICTED: Mesocricetus auratus sterol-C5-desaturase (Sc5d), mRNA	424	6e-114	XM_005069403
Cricetulus griseus (Chinese hamster) [rodents]			
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	396	1e-105	XM_007651891
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	396	1e-105	XM_003511371
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	392	2e-104	XM_027411877
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	392	2e-104	XM_027411876
RNA interference vector psiCHECK(TM)-2 [other sequences]			
RNA interference vector psiCHECK(TM)-2, complete sequence	252	3e-62	AY535007
RNA interference vector psiCHECK(TM)-1 [other sequences]			
RNA interference vector psiCHECK(TM)-1, complete sequence	252	3e-62	AY535006
Co-reporter vector phRL-CMV [other sequences]			
Co-reporter vector phRL-CMV, complete sequence	231	4e-56	AF362549
Co-reporter vector phRL-SV40 [other sequences]			
Co-reporter vector phRL-SV40, complete sequence	231	4e-56	AF362548

Description	Score	E value	Accession
Co-reporter vector phRL-TK(Int-) [other sequences]			
Co-reporter vector phRL-TK(Int-), complete sequence	231	4e-56	**AF362547**
Co-reporter vector phRL-null [other sequences]			
Co-reporter vector phRL-null, complete sequence	231	4e-56	**AF362546**
Co-reporter vector pHRL-TK [other sequences]			
Co-reporter vector pHRL-TK, complete sequence	231	4e-56	**AF362545**
Renilla luciferase reporter vector pGL4.75[hRluc/CMV] [other sequences]			
Renilla luciferase reporter vector pGL4.75[hRluc/CMV], complete sequence	228	5e-55	**AY738231**
Renilla luciferase reporter vector pGL4.74[hRluc/TK] [other sequences]			
Renilla luciferase reporter vector pGL4.74[hRluc/TK], complete sequence	228	5e-55	**AY738230**
Renilla luciferase reporter vector pGL4.73[hRluc/SV40] [other sequences]			
Renilla luciferase reporter vector pGL4.73[hRluc/SV40], complete sequence	228	5e-55	**AY738229**
Renilla luciferase reporter vector pGL4.70[hRluc] [other sequences]			
Renilla luciferase reporter vector pGL4.70[hRluc], complete sequence	228	5e-55	**AY738226**
Co-reporter vector phRG-TK [other sequences]			
Co-reporter vector phRG-TK, complete sequence	228	5e-55	**AF362551**
Co-reporter vector phRG-B [other sequences]			
Co-reporter vector phRG-B, complete sequence	228	5e-55	**AF362550**
Renilla luciferase reporter vector pGL4.82[hRluc/Puro] [other sequences]			
Synthetic Renilla luciferase reporter vector pGL4.82[hRluc/Puro], complete sequence	228	5e-55	**DQ188846**
Renilla luciferase reporter vector pGL4.79[hRluc/Neo] [other sequences]			
Renilla luciferase reporter vector pGL4.79[hRluc/Neo], complete sequence	228	5e-55	**DQ188843**
Luciferase reporter vector pGL4.76[hRluc/Hygro] [other sequences]			
Luciferase reporter vector pGL4.76[hRluc/Hygro], complete sequence	228	5e-55	**AY864931**
Cloning vector pT7 RL2 [other sequences]			
Cloning vector pT7 RL2, complete sequence	217	1e-51	**KM099240**
Cloning vector pT7_RL1 [other sequences]			
Cloning vector pT7_RL1, complete sequence	217	1e-51	**KM099239**
Renilla luciferase reporter vector pGL4.72[hRlucCP] [other sequences]			
Renilla luciferase reporter vector pGL4.72[hRlucCP], complete sequence	217	1e-51	**AY738228**
Renilla luciferase reporter vector pGL4.71[hRlucP] [other sequences]			
Renilla luciferase reporter vector pGL4.71[hRlucP], complete sequence	217	1e-51	**AY738227**
Reporter vector phRG(R2.2) [other sequences]			
Reporter vector phRG(R2.2), complete sequence	217	1e-51	**AY487824**
Reporter vector phRG(R2.1) [other sequences]			
Reporter vector phRG(R2.1), complete sequence	217	1e-51	**AY487823**
Renilla luciferase reporter vector pGL4.84[hRlucCP/Puro] [other sequences]			
Synthetic Renilla luciferase reporter vector pGL4.84[hRlucCP/Puro], complete sequence	217	1e-51	**DQ188848**
Renilla luciferase reporter vector pGL4.83[hRlucP/Puro] [other sequences]			
Synthetic Renilla luciferase reporter vector pGL4.83[hRlucP/Puro], complete sequence	217	1e-51	**DQ188847**
Renilla luciferase reporter vector pGL4.81[hRlucCP/Neo] [other sequences]			
Synthetic Renilla luciferase reporter vector pGL4.81[hRlucCP/Neo], complete sequence	217	1e-51	**DQ188845**

Description	Score	E value	Accession
Renilla luciferase reporter vector pGL4.80[hRlucP/Neo] [other sequences]			
Synthetic Renilla luciferase reporter vector pGL4.80[hRlucP/Neo], complete sequence	217	1e-51	**DQ188844**
Luciferase reporter vector pGL4.78[hRlucCP/Hygro] [other sequences]			
Luciferase reporter vector pGL4.78[hRlucCP/Hygro], complete sequence	217	1e-51	**AY864933**
Luciferase reporter vector pGL4.77[hRlucP/Hygro] [other sequences]			
Luciferase reporter vector pGL4.77[hRlucP/Hygro], complete sequence	217	1e-51	**AY864932**
Plant expression vector pDuExB2 (pDuExD7) [other sequences]			
Plant expression vector pDuExB2 (pDuExD7), complete sequence	213	1e-50	**EF565885**
Plant expression vector pDuExB (pDuExDc6) [other sequences]			
Plant expression vector pDuExB (pDuExDc6), complete sequence	213	1e-50	**EF565884**
synthetic construct [other sequences]			
Synthetic construct clone Den3-E24 Rluc-ubiquitin-neo fusion protein and polyprotein genes, complete cds	211	5e-50	**KM222446**
Synthetic construct clone Den3-E21 Rluc-ubiquitin-neo fusion protein and polyprotein genes, complete cds	211	5e-50	**KM222445**
Synthetic construct gene for mKusabiraOrangeKappa-RLuc8.6, complete cds	206	2e-48	**LC033422**
Synthetic construct gene for mKusabiraOrange1-RLuc8.6, complete cds	206	2e-48	**LC033416**
Synthetic construct gene for mCherry(delC13)-RLuc8.6(delN6), complete cds	206	2e-48	**LC033414**
Synthetic construct gene for mCherry(delC13)-RLuc8.6(delN5), complete cds	206	2e-48	**LC033413**
Synthetic construct gene for mCherry(delC13)-RLuc8.6(delN4), complete cds	206	2e-48	**LC033412**
Synthetic construct gene for mCherry(delC12)-RLuc8.6(delN6), complete cds	206	2e-48	**LC033411**
Synthetic construct gene for mCherry(delC12)-RLuc8.6(delN5), complete cds	206	2e-48	**LC033410**
Synthetic construct gene for mCherry(delC12)-RLuc8.6(delN4), complete cds	206	2e-48	**LC033409**
Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6(delN6), complete cds	206	2e-48	**LC033408**
Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6(delN5), complete cds	206	2e-48	**LC033407**
Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6(delN4), complete cds	206	2e-48	**LC033406**
Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6, complete cds	206	2e-48	**LC033405**
Synthetic construct gene for mCherry(delC10)-Orange-Nano-lantern, complete cds	206	2e-48	**LC033404**
Synthetic construct gene for Che(dC10-sC2)-RL8m1, complete cds	206	2e-48	**LC033401**
Synthetic construct gene for Che(dC10-sC1)-RL8m1, complete cds	206	2e-48	**LC033400**
Synthetic construct gene for Orange-Nano-lantern(Ca2+)-H2B, complete cds	206	2e-48	**AB983217**
Synthetic construct gene for Orange-Nano-lantern(Ca2+), complete cds	206	2e-48	**AB983216**
Synthetic construct gene for TurboFP650-RLuc8.6-545, complete cds	206	2e-48	**AB982104**
Synthetic construct gene for TurboFP635-RLuc8.6, complete cds	206	2e-48	**AB982103**
Synthetic construct gene for TurboFP635-RLuc8.6-545, complete cds	206	2e-48	**AB982102**
Synthetic construct gene for tdTomato-RLuc8.6, complete cds	206	2e-48	**AB982100**
Synthetic construct gene for TagRFP-RLuc8.6, complete cds	206	2e-48	**AB982098**
Synthetic construct gene for mRuby2-RLuc8.6, complete cds	206	2e-48	**AB982096**
Synthetic construct gene for mOrange2-RLuc8.6, complete cds	206	2e-48	**AB982095**
Synthetic construct gene for mKusabiraOrange2(delC5)-RLuc8.6, complete cds	206	2e-48	**AB982094**
Synthetic construct gene for mKusabiraOrange2(delC4)-RLuc8.6, complete cds	206	2e-48	**AB982093**
Synthetic construct gene for mKusabiraOrange2(delC3)-RLuc8.6, complete cds	206	2e-48	**AB982092**
Synthetic construct gene for mKusabiraOrange2(delC2)-RLuc8.6, complete cds	206	2e-48	**AB982091**
Cloning vector pCRm-Rluc-PHLEO [other sequences]			

Description	Score	E value	Accession
Cloning vector pCRm-Rluc-PHLEO, complete sequence	211	5e-50	**KF035117**
Cloning vector pCRm-Rluc-PAC　　　[other sequences　　]			
Cloning vector pCRm-Rluc-PAC, complete sequence	211	5e-50	**KF035116**
Cloning vector pCRm-Rluc-NEO　　　[other sequences　　]			
Cloning vector pCRm-Rluc-NEO, complete sequence	211	5e-50	**KF035115**
Cloning vector pCRm-Rluc-HYG　　　[other sequences　　]			
Cloning vector pCRm-Rluc-HYG, complete sequence	211	5e-50	**KF035114**
Cloning vector pCRm-Rluc-BSD　　　[other sequences　　]			
Cloning vector pCRm-Rluc-BSD, complete sequence	211	5e-50	**KF035113**
Hepatitis C virus replicon 4a ED43-RlucNeo (R+I)　　　[other sequences　　]			
Hepatitis C virus replicon 4a ED43-RlucNeo (R+I), complete sequence	211	5e-50	**JX885981**
Biobrick cloning vector BBa_J96034　　　[other sequences　　]			
Biobrick cloning vector BBa_J96034, complete sequence	211	5e-50	**JN204887**
Cloning vector pDuExDn6　　　[other sequences　　]			
Cloning vector pDuExDn6, complete sequence	211	5e-50	**GU370779**
Cloning vector pBIND-GR　　　[other sequences　　]			
Cloning vector pBIND-GR, complete sequence	211	5e-50	**GQ229580**
Cloning vector pBIND-ER (alpha)　　　[other sequences　　]			
Cloning vector pBIND-ER (alpha), complete sequence	211	5e-50	**GQ229579**
Cloning vector pFN26A (BIND) hRluc-neo　　　[other sequences　　]			
Cloning vector pFN26A (BIND) hRluc-neo, complete sequence	211	5e-50	**GQ229578**
Cloning vector pmirGLO　　　[other sequences　　]			
Cloning vector pmirGLO, complete sequence	211	5e-50	**FJ376737**
CMV hRluc-neo Flexi Vector pF9A　　　[other sequences　　]			
CMV hRluc-neo Flexi Vector pF9A, complete sequence	211	5e-50	**DQ871024**

- ○ **Taxonomy**

Taxonomy	Number of hits	Number of Organisms	Description
root	101	50	
. Muroidea	28	6	
.. Murinae	23	4	
... Mus	19	3	
.... Mus	16	2	
..... Mus musculus	13	1	**Mus musculus hits**
..... Mus caroli	3	1	**Mus caroli hits**
.... Mus pahari	3	1	**Mus pahari hits**
... Rattus norvegicus	4	1	**Rattus norvegicus hits**
.. Cricetinae	5	2	
... Mesocricetus auratus	1	1	**Mesocricetus auratus hits**
... Cricetulus griseus	4	1	**Cricetulus griseus hits**
. artificial sequences	73	44	

.. vectors	43	43	
... RNA interference vector psiCHECK(TM)-2	1	1	**RNA interference vector psiCHECK(TM)-2 hits**
... RNA interference vector psiCHECK(TM)-1	1	1	**RNA interference vector psiCHECK(TM)-1 hits**
... Co-reporter vector phRL-CMV	1	1	**Co-reporter vector phRL-CMV hits**
... Co-reporter vector phRL-SV40	1	1	**Co-reporter vector phRL-SV40 hits**
... Co-reporter vector phRL-TK(Int-)	1	1	**Co-reporter vector phRL-TK(Int-) hits**
... Co-reporter vector phRL-null	1	1	**Co-reporter vector phRL-null hits**
... Co-reporter vector pHRL-TK	1	1	**Co-reporter vector pHRL-TK hits**
... Renilla luciferase reporter vector pGL4.75[hRluc/CMV]	1	1	**Renilla luciferase reporter vector pGL4.75[hRluc/CMV] hits**
... Renilla luciferase reporter vector pGL4.74[hRluc/TK]	1	1	**Renilla luciferase reporter vector pGL4.74[hRluc/TK] hits**
... Renilla luciferase reporter vector pGL4.73[hRluc/SV40]	1	1	**Renilla luciferase reporter vector pGL4.73[hRluc/SV40] hits**
... Renilla luciferase reporter vector pGL4.70[hRluc]	1	1	**Renilla luciferase reporter vector pGL4.70[hRluc] hits**
... Co-reporter vector phRG-TK	1	1	**Co-reporter vector phRG-TK hits**
... Co-reporter vector phRG-B	1	1	**Co-reporter vector phRG-B hits**
... eukaryotic vectors	6	6	
.... Renilla luciferase reporter vector pGL4.82[hRluc/Puro]	1	1	**Renilla luciferase reporter vector pGL4.82[hRluc/Puro] hits**
.... Renilla luciferase reporter vector pGL4.79[hRluc/Neo]	1	1	**Renilla luciferase reporter vector pGL4.79[hRluc/Neo] hits**
.... Renilla luciferase reporter vector pGL4.84[hRlucCP/Puro]	1	1	**Renilla luciferase reporter vector pGL4.84[hRlucCP/Puro] hits**
.... Renilla luciferase reporter vector pGL4.83[hRlucP/Puro]	1	1	**Renilla luciferase reporter vector pGL4.83[hRlucP/Puro] hits**
.... Renilla luciferase reporter vector pGL4.81[hRlucCP/Neo]	1	1	**Renilla luciferase reporter vector pGL4.81[hRlucCP/Neo] hits**
.... Renilla luciferase reporter vector pGL4.80[hRlucP/Neo]	1	1	**Renilla luciferase reporter vector pGL4.80[hRlucP/Neo] hits**
... Luciferase reporter vector pGL4.76[hRluc/Hygro]	1	1	**Luciferase reporter vector pGL4.76[hRluc/Hygro] hits**
... Cloning vector pT7 RL2	1	1	**Cloning vector pT7 RL2 hits**
... Cloning vector pT7_RL1	1	1	**Cloning vector pT7_RL1 hits**
... Renilla luciferase reporter vector pGL4.72[hRlucCP]	1	1	**Renilla luciferase reporter vector pGL4.72[hRlucCP] hits**
... Renilla luciferase reporter vector pGL4.71[hRlucP]	1	1	**Renilla luciferase reporter vector pGL4.71[hRlucP] hits**
... Reporter vector phRG(R2.2)	1	1	**Reporter vector phRG(R2.2) hits**
... Reporter vector phRG(R2.1)	1	1	**Reporter vector phRG(R2.1) hits**
... Luciferase reporter vector pGL4.78[hRlucCP/Hygro]	1	1	**Luciferase reporter vector pGL4.78[hRlucCP/Hygro] hits**
... Luciferase reporter vector pGL4.77[hRlucP/Hygro]	1	1	**Luciferase reporter vector pGL4.77[hRlucP/Hygro] hits**
... Plant expression vector pDuExB2 (pDuExD7)	1	1	**Plant expression vector pDuExB2 (pDuExD7) hits**
... Plant expression vector pDuExB (pDuExDc6)	1	1	**Plant expression vector pDuExB (pDuExDc6) hits**
... Cloning vector pCRm-Rluc-PHLEO	1	1	**Cloning vector pCRm-Rluc-PHLEO hits**
... Cloning vector pCRm-Rluc-PAC	1	1	**Cloning vector pCRm-Rluc-PAC hits**
... Cloning vector pCRm-Rluc-NEO	1	1	**Cloning vector pCRm-Rluc-NEO hits**
... Cloning vector pCRm-Rluc-HYG	1	1	**Cloning vector pCRm-Rluc-HYG hits**
... Cloning vector pCRm-Rluc-BSD	1	1	**Cloning vector pCRm-Rluc-BSD hits**

... Hepatitis C virus replicon 4a ED43-RlucNeo (R+I)	1	1	**Hepatitis C virus replicon 4a ED43-RlucNeo (R+I) hits**
... Biobrick cloning vector BBa_J96034	1	1	**Biobrick cloning vector BBa_J96034 hits**
... Cloning vector pDuExDn6	1	1	**Cloning vector pDuExDn6 hits**
... Cloning vector pBIND-GR	1	1	**Cloning vector pBIND-GR hits**
... Cloning vector pBIND-ER (alpha)	1	1	**Cloning vector pBIND-ER (alpha) hits**
... Cloning vector pFN26A (BIND) hRluc-neo	1	1	**Cloning vector pFN26A (BIND) hRluc-neo hits**
... Cloning vector pmirGLO	1	1	**Cloning vector pmirGLO hits**
... CMV hRluc-neo Flexi Vector pF9A	1	1	**CMV hRluc-neo Flexi Vector pF9A hits**
.. synthetic construct	30	1	**synthetic construct hits**

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